

Amendments to the Specification

Please replace the paragraph beginning at page 4, line 14, with the following rewritten paragraph:

Figures 1A-B: Similarity of PAGE-4, GAGE and MAGE: (A) The predicted PAGE-4 reading frame is derived from the full length PAGE-4 EST clone nh32cO6. The GAGE and MAGE sequences are from SW: GGE1, GGE2, GGE3, GGE4, GGE5, GGE6, MAG5 and MAG8~HUMAN. Note that the "MAGE-alignment" matches amino acids that occur in MAGE5 and/or MAGE8, which are similar to PAGE-4 and/or GAGE1-6; the homologies between single members of the MAGE and PAGE and GAGE protein families are weaker. (B) Alignment of PAGE-4 with other PAGEs. PAGE-2 was translated from the EST ai61aO4 EST-cluster and PAGE-3 from om29fO8. PAGE-3 was translated from one single EST and it is possible that the truncated amino terminus results from a sequence artifact (the homology extends further to the N-terminus in another reading frame). Several other so far undefined EST clusters were found that have homology to PAGE as well as to GAGE. These clusters do not have the striking similarities that the other GAGE family members have to each other, but they are also not significantly more similar to PAGE than to GAGE. Representatives of some of these cDNA clusters are the ESTS yd88el 1 (fetal liver/spleen), yw86aO6 (placenta) and yi21hO1 (placenta).

Please replace the paragraph beginning at page 4, line 31, with the following rewritten paragraph:

Figures 2A-C: Hybridization analysis of PAGE-4 expression: (A) A MTN Dot blot (left) and Northern blots (middle to right) were probed with a 140 bp ³²P labeled PAGE-4 probe under very stringent hybridization conditions (50% formamide, 55 C). Specific